#3

PAGE: 1

RAW SEQUENCE LISTING PATENT APPLICATION US/08/113,561

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·	SEQUENCE LISTING
(1) G	deneral Information:
(i)	APPLICANTS: Adams, Thomas R. et al.
(ii)	SEQUENCE LISTING General Information: APPLICANTS: Adams, Thomas R. et al. TITLE OF INVENTION: Methods and Compositions for the Production of Stably Transformed, Fertile, Monocot Plants and Cells Thereof
(iii)	NUMBER OF SEQUENCES: 13
(iv)	CORRESPONDENCE ADDRESS: (A) ADDRESSEE: Arnold, White & Durkee (B) STREET: P.O. BOX 4433 (C) CITY: Houston (D) STATE: TX (E) COUNTRY: USA (F) ZIP: 77210
(v)	COMPUTER READABLE FORM: (A) MEDIUM TYPE: Floppy disk (B) COMPUTER: IBM PC compatible (C) OPERATING SYSTEM: PC-DOS/MS-DOS (D) SOFTWARE: Patent In Release #1.0, Version #1.25
(vi)	CURRENT APPLICATION DATA: (A) APPLICATION NUMBER: unknown (B) FILING DATE: August 25, 1993 (C) CLASSIFICATION: unknown
(viii)	ATTORNEY/AGENT INFORMATION: (A) NAME: Parker, David L. (B) REGISTRATION NUMBER: 32,165 (C) REFERENCE/DOCKET NUMBER: DEKA:055/PAR
(ix)	TELECOMMUNICATION INFORMATION: (A) TELEPHONE: 512-320-7200 (B) TELEFAX: 512-474-7577 (C) TELEX: NOT APPLICABLE
(2) INFO	RMATION FOR SEQ ID NO:1:
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 15 amino acid residues (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1:

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52		
3 Met	Ala Thr Val Pro Glu Leu Asn Cys Glu Met Pro Pro Ser Asp	
54 1	. 5 10 15	
55		
56		
	INFORMATION FOR SEQ ID NO:2:	
58	(1)	
59	(i) SEQUENCE CHARACTERISTICS:	
0	(A) LENGTH: 35 base pairs	
L 2	(B) TYPE: nucleic acid (C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
	(b) Toronogi. Timeat	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:	
	(AI) DEGOLACE DESCRIPTION. DEG 15 NO.2.	
GAG	GATCCGT CGACATGGTA AGCTTAGCGG GCCCC	35
(2)	INFORMATION FOR SEQ ID NO:3:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 29 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
	(') 67677767 7766777777 676 77 17 17	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:	
CAM	CCGTCGA CCATGGCGCT TCAAGCTTC	
GAI	29	
(2)	INFORMATION FOR SEQ ID NO:4:	
	~	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 29 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:	
007	COMMON COCCON COMM CON ACCOMM	
GCA	GCTGGTA CCGCGAAGTT CGAAGGGCT	
	29	
(2)	INFORMATION FOR SEQ ID NO:5:	
(2)	INICIALIZATION FOR DBY ID NO.3.	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 49 base pairs	
	(B) TYPE: pucleic acid	

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103 104	(C) STRANDEDNESS: single (D) TOPOLOGY: linear	
105 106	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:	
107	(XI) SEQUENCE DESCRIPTION: SEQ ID NO:5:	
109 110	AGACAACA AAGCAGCAAC CATGGCCAGC ATGCAAGGCC TCATGCATC	49
111 112 (2) 113	INFORMATION FOR SEQ ID NO:6:	
114 115 116 117 118	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 49 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
120 121	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:	
	GGGATGCA TGAGGCCTTG CATGCTGGCC ATGGTTGCTG CTTTGTTGT	
123 124 125	49	
126 (2) 127	INFORMATION FOR SEQ ID NO:7:	
128 129 130 131 132 133	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 11 amino acid residues (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
134 135	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:	
136 Met 137 1 138	Ala Ser Met Gln Gly Leu Met His Pro Gly 5 10	
139 140 (2) 141	INFORMATION FOR SEQ ID NO:8:	
141 142 143 144 145 146	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 6 amino acid residues (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
148 149	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:	
	Lys Cys Met Gln Val 5	

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154 155	(2)	INF	ORMA!	rion	FOR	SEQ	ID 1	NO : 9	:							
156		(i)	SEC	OUEN	CE CI	HARA	CTER	ISTI	CS:							
157			(1	A) LI	ENGTI	H: 18	3 bas	se pa	airs							
158					YPE:			_								
159			((c) s:	[RAN]	DEDNI	ESS:	sing	gle							
160			(1) T(OPOL	OGY:	line	ear								
161																
162		(xi)	SE	QUEN	CE DI	ESCR:	IPTI	ON: S	SEQ I	D NO	0:9:					
163																
164	AAG	JGAA(GUG A	AAGU(GAAG											
165		18														
166																
167																
168	(2)	INF	ORMA'	rion	FOR	SEQ	ID 1	NO:10):							
169																
170		(i)		-	CE CE											
171					ENGTI					rs.						
172					YPE:											
173					rani			-	Jle							
174			(I) T(OPOLO	OGY:	line	ear								
175																
176		(ii)	MOI	LECUI	LE T	PE:	DNA	(gei	omic	2)						
177																
178		(ix)	FEA													
179			()	A) N2	ME/I	CEV.	מחס									
180					CAT:			1839								
181			(1	3) L(OCAT:	ON:	1									
181 182		(xi)	(1	3) L(ON:	1		SEQ 1	ID NO	D:10:	:				
181 182 183			(I SEÇ	OUENO	CE DI	ION:	11 [PTIC	ON: S								ama.
181 182	ATG		(I SEÇ	OUENO	CE DI	ION:	11 [PTIC	ON: S					TAC	ААТ	TGC	CTC
181 182 183 184		GAT 48	(I SE(AAC	B) LO QUENO AAT	OCAT: CE DI CCG	ION: ESCRI AAC	1I	ON: S	GAA	TGC	ATT	CCT			TGC Cys	
181 182 183 184 185		GAT 48	(I SE(AAC	B) LO QUENO AAT	OCAT: CE DI CCG	ION: ESCRI AAC	1I	ON: S	GAA	TGC	ATT	CCT				
181 182 183 184 185 186 187	Met 1	GAT 48 Asp	(I SEÇ AAC Asn	3) LO QUENO AAT Asn	CE DI CCG Pro 5	ION: ESCR: AAC Asn	11 IPTIC ATC Ile	ON: S AAT Asn	GAA Glu	TGC Cys 10	ATT Ile	CCT Pro	Tyr	Asn	Cys 15	Leu
181 182 183 184 185 186 187 188	Met 1	GAT 48 Asp	(I SEÇ AAC Asn	3) LO QUENO AAT Asn	CE DI CCG Pro 5	ION: ESCR: AAC Asn	11 IPTIC ATC Ile	ON: S AAT Asn	GAA Glu	TGC Cys 10	ATT Ile	CCT Pro	Tyr	Asn	Cys	Leu
181 182 183 184 185 186 187 188 189	Met 1 AGC	GAT 48 Asp AAC 96	(I SE(AAC Asn CCT	QUENC AAT Asn GAA	CCG Pro 5	ESCR: AAC Asn GAA	11 IPTIC ATC Ile GTG	ON: S AAT Asn CTG	GAA Glu GGT	TGC Cys 10 GGC	ATT Ile GAA	CCT Pro CGC	Tyr ATC	Asn GAA	Cys 15 ACC	Leu GGT
181 182 183 184 185 186 187 188 189 190	Met 1 AGC	GAT 48 Asp AAC 96	(I SE(AAC Asn CCT	QUENC AAT Asn GAA	CCG Pro 5	ESCR: AAC Asn GAA	11 IPTIC ATC Ile GTG	ON: S AAT Asn CTG	GAA Glu GGT Gly	TGC Cys 10 GGC	ATT Ile GAA	CCT Pro CGC	Tyr ATC	Asn GAA Glu	Cys 15	Leu GGT
181 182 183 184 185 186 187 188 189 190 191	Met 1 AGC	GAT 48 Asp AAC 96	(I SE(AAC Asn CCT	QUENC AAT Asn GAA	CCG Pro 5	ESCR: AAC Asn GAA	11 IPTIC ATC Ile GTG	ON: S AAT Asn CTG	GAA Glu GGT	TGC Cys 10 GGC	ATT Ile GAA	CCT Pro CGC	Tyr ATC	Asn GAA	Cys 15 ACC	Leu GGT
181 182 183 184 185 186 187 188 189 190 191 192	Met 1 AGC Ser	GAT 48 Asp AAC 96 Asn	SE(AAC Asn CCT	QUENC AAT Asn GAA Glu 20	CCG Pro 5 GTG	ESCRI AAC Asn GAA	II IPTIC ATC Ile GTG Val	ON: S AAT Asn CTG	GAA Glu GGT Gly 25	TGC Cys 10 GGC Gly	ATT Ile GAA Glu	CCT Pro CGC Arg	Tyr ATC Ile	Asn GAA Glu 30	Cys 15 ACC Thr	Leu GGT Gly
181 182 183 184 185 186 187 188 189 190 191 192 193	Met 1 AGC Ser	GAT 48 Asp AAC 96 Asn	SE(AAC Asn CCT	QUENC AAT Asn GAA Glu 20	CCG Pro 5 GTG	ESCRI AAC Asn GAA	II IPTIC ATC Ile GTG Val	ON: S AAT Asn CTG	GAA Glu GGT Gly 25	TGC Cys 10 GGC Gly	ATT Ile GAA Glu	CCT Pro CGC Arg	Tyr ATC Ile	Asn GAA Glu 30	Cys 15 ACC	Leu GGT Gly
181 182 183 184 185 186 187 188 189 190 191 192 193 194 195	Met 1 AGC Ser	GAT 48 Asp AAC 96 Asn ACC	SEG AAC Asn CCT Pro	QUENC AAT ASN GAA Glu 20	CCG CCG Pro 5 GTG Val	ESCR: AAC Asn GAA Glu ATT	1I IPTIC ATC Ile GTG Val	AAT Asn CTG Leu CTG	GAA Glu GGT Gly 25 TCC	TGC Cys 10 GGC Gly CTG	ATT Ile GAA Glu ACC	CCT Pro CGC Arg	Tyr ATC Ile	Asn GAA Glu 30 CTG	Cys 15 ACC Thr	Leu GGT Gly AGC
181 182 183 184 185 186 187 188 189 190 191 192 193 194 195	Met 1 AGC Ser	GAT 48 Asp AAC 96 Asn ACC	SEG AAC Asn CCT Pro CCA	QUENC AAT ASN GAA Glu 20	CCG CCG Pro 5 GTG Val	ESCR: AAC Asn GAA Glu ATT	1I IPTIC ATC Ile GTG Val	AAT Asn CTG Leu CTG	GAA Glu GGT Gly 25 TCC	TGC Cys 10 GGC Gly CTG	ATT Ile GAA Glu ACC	CCT Pro CGC Arg	Tyr ATC Ile TTT Phe	Asn GAA Glu 30 CTG	Cys 15 ACC Thr	Leu GGT Gly
181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197	Met 1 AGC Ser	GAT 48 Asp AAC 96 Asn ACC	SEG AAC Asn CCT Pro	QUENC AAT ASN GAA Glu 20	CCG CCG Pro 5 GTG Val	ESCR: AAC Asn GAA Glu ATT	1I IPTIC ATC Ile GTG Val	AAT Asn CTG Leu CTG	GAA Glu GGT Gly 25 TCC	TGC Cys 10 GGC Gly CTG	ATT Ile GAA Glu ACC	CCT Pro CGC Arg	Tyr ATC Ile	Asn GAA Glu 30 CTG	Cys 15 ACC Thr	Leu GGT Gly AGC
181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197	Met 1 AGC Ser TAC	GAT 48 Asp AAC 96 Asn ACC	SEG AAC Asn CCT Pro CCA Pro 35	QUENC AAT ASN GAA Glu 20 ATC	CCG CCG Pro 5 GTG Val GAT Asp	ESCR: AAC Asn GAA Glu ATT Ile	1 IPTIC ATC Ile GTG Val TCC Ser	AAT Asn CTG Leu CTG Leu 40	GAA Glu GGT Gly 25 TCC Ser	TGC Cys 10 GGC Gly CTG Leu	ATT Ile GAA Glu ACC Thr	CCT Pro CGC Arg CAA Gln	Tyr ATC Ile TTT Phe 45	Asn GAA Glu 30 CTG Leu	Cys 15 ACC Thr CTG Leu	Leu GGT Gly AGC Ser
181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198	Met 1 AGC Ser TAC Tyr	GAT 48 Asp AAC 96 Asn ACC 144 Thr	SEG AAC Asn CCT Pro CCA Pro 35	QUENC AAT ASN GAA Glu 20 ATC	CCG CCG Pro 5 GTG Val GAT Asp	ESCR: AAC Asn GAA Glu ATT Ile	1 IPTIC ATC Ile GTG Val TCC Ser	AAT Asn CTG Leu CTG Leu 40	GAA Glu GGT Gly 25 TCC Ser	TGC Cys 10 GGC Gly CTG Leu	ATT Ile GAA Glu ACC Thr	CCT Pro CGC Arg CAA Gln	Tyr ATC Ile TTT Phe 45	Asn GAA Glu 30 CTG Leu	Cys 15 ACC Thr	Leu GGT Gly AGC Ser
181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200	Met 1 AGC Ser TAC Tyr	GAT 48 Asp AAC 96 Asn ACC 144 Thr	SEG AAC Asn CCT Pro CCA Pro 35	QUENC AAT ASN GAA Glu 20 ATC Ile	CCAT: CCG Pro 5 GTG Val GAT Asp	ESCR: AAC Asn GAA Glu ATT Ile GCT	ATC Ile GTG Val TCC Ser	AAT Asn CTG Leu CTG Leu 40	GAA Glu GGT Gly 25 TCC Ser	TGC Cys 10 GGC Gly CTG Leu CTG	ATT Ile GAA Glu ACC Thr	CCT Pro CGC Arg CAA Gln CTG	Tyr ATC Ile TTT Phe 45 GTG	Asn GAA Glu 30 CTG Leu GAT	Cys 15 ACC Thr CTG Leu	Leu GGT Gly AGC Ser
181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201	Met 1 AGC Ser TAC Tyr	GAT 48 Asp AAC 96 Asn ACC 144 Thr	SEG AAC Asn CCT Pro CCA Pro 35	QUENC AAT ASN GAA Glu 20 ATC Ile	CCAT: CCG Pro 5 GTG Val GAT Asp	ESCR: AAC Asn GAA Glu ATT Ile GCT	ATC Ile GTG Val TCC Ser GGC Gly	AAT Asn CTG Leu CTG Leu 40	GAA Glu GGT Gly 25 TCC Ser	TGC Cys 10 GGC Gly CTG Leu CTG	ATT Ile GAA Glu ACC Thr	CCT Pro CGC Arg CAA Gln CTG Leu	Tyr ATC Ile TTT Phe 45 GTG	Asn GAA Glu 30 CTG Leu GAT	Cys 15 ACC Thr CTG Leu	Leu GGT Gly AGC Ser
181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202	Met 1 AGC Ser TAC Tyr	GAT 48 Asp AAC 96 Asn ACC 144 Thr	SEG AAC Asn CCT Pro CCA Pro 35	QUENC AAT ASN GAA Glu 20 ATC Ile	CCAT: CCG Pro 5 GTG Val GAT Asp	ESCR: AAC Asn GAA Glu ATT Ile GCT	ATC Ile GTG Val TCC Ser	AAT Asn CTG Leu CTG Leu 40	GAA Glu GGT Gly 25 TCC Ser	TGC Cys 10 GGC Gly CTG Leu CTG	ATT Ile GAA Glu ACC Thr	CCT Pro CGC Arg CAA Gln CTG	Tyr ATC Ile TTT Phe 45 GTG	Asn GAA Glu 30 CTG Leu GAT	Cys 15 ACC Thr CTG Leu	Leu GGT Gly AGC Ser
181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201	Met 1 AGC Ser TAC Tyr GAA Glu	GAT 48 Asp AAC 96 Asn ACC 144 Thr TTT 192 Phe 50	SEG AAC Asn CCT Pro CCA Pro 35 GTG Val	QUENC AAT Asn GAA Glu 20 ATC Ile CCC	CCAT: CCG Pro 5 GTG Val GAT Asp GGT Gly	ESCR: AAC Asn GAA Glu ATT Ile GCT Ala	TCC Ser GGC Gly 55	AAT Asn CTG Leu CTG Leu 40 TTT	GAA Glu GGT Gly 25 TCC Ser GTG Val	TGC Cys 10 GGC Gly CTG Leu CTG	ATT Ile GAA Glu ACC Thr GGC Gly	CCT Pro CGC Arg CAA Gln CTG Leu 60	Tyr ATC Ile TTT Phe 45 GTG Val	Asn GAA Glu 30 CTG Leu GAT Asp	Cys 15 ACC Thr CTG Leu	Leu GGT Gly AGC Ser ATC

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205	240														
206	Trp Gly	Tle	Dhe	Glv	Dro	Sar	Gln	Trn	Δen	λla	Dhe	T.611	Va l	Gln	Tla
207	65			017	70	DCI	0111	115	пор	75	1110	пси	vai	0111	80
208	03				, 0					, 5					00
209	GAA CAG	CTG	ATT	AAC	CAA	CGC	ATC	GAA	GAA	TTC	GCT	AGG	AAC	CAA	GCC
210	288								 .		-			····	
211	Glu Gln	Leu	Ile	Asn	Gln	Arq	Ile	Glu	Glu	Phe	Ala	Arq	Asn	Gln	Ala
212				85					90			5		95	
213															
214	ATT TCC	CGC	CTG	GAA	GGC	CTG	AGC	AAT	CTG	TAC	CAA	ATT	TAC	GCC	GAA
215	336														
216	Ile Ser	Arg	Leu	Glu	Gly	Leu	Ser	Asn	Leu	Tyr	Gln	Ile	Tyr	Ala	Glu
217		_	100		_			105		_			110		
218															
219	TCC TTT	CGC	GAG	TGG	GAA	GCC	GAT	CCT	ACC	AAT	CCA	GCC	CTG	CGC	GAA
220	384														
221	Ser Phe	Arg	Glu	Trp	Glu	Ala	Asp	${\tt Pro}$	Thr	Asn	Pro	Ala	Leu	Arg	Glu
222		115					120					125			
223															
224	GAG ATG	CGC	ATT	CAA	TTC	AAT	GAC	ATG	AAC	AGC	GCC	CTG	ACC	ACC	GCT
225	432										_		_	_	_
226	Glu Met	Arg	Ile	Gln	Phe		Asp	Met	Asn	Ser		Leu	Thr	Thr	Ala
227	130					135					140				
228															
229	ATT CCT	CTG	TTT	GCC	GTG	CAA	AAT	TAC	CAA	GTG	CCT	CTG	CTG	TCC	GTG
230	480		D1		77-7	~1	*	m	~ 1	TT - 7	D	.	7	a	**- 7
231	Ile Pro	ьeu	Pne	Ата		GIN	Asn	Tyr	GIN		Pro	ьeu	ьeu	ser	
232	145				150					155					160
233	mag ama	C1 2 2	aam	aaa	7 7 M	OTTO	CI N ITT	CITIC	maa	аша	CITIC	aaa	CAM	CITIC	maa.
234 235	TAC GTG 528	CAA	GCT	GCC	AAT	CIG	CAI	CIG	100	GIG	CIG	CGC	GAI	GIG	ICC
236	Tyr Val	Gln	712	712	Aan	Lau	Wic	Lou	Cor	17a 1	Lou	λνα	λcn	1721	Ser
237	Iyi vai	GIII	AIA	165	ASII	пеп	птъ	пец	170	vai	пеа	Arg	Азр	175	Ser
238				103					170					113	
239	GTG TTT	GGC	CAA	ΔGG	тсс	GGC	արար	СΔТ	GCC	GCC	ACC	ΔΤΟ	ממ	AGC	CGC
240	576	-	0111	1100		-		0111	-	-		••••			-
241	Val Phe	Glv	Gln	Ara	Trp	Glv	Phe	Asp	Ala	Ala	Thr	Ile	Asn	Ser	Arg
242		1	180	5		1		185					190		5
243															
244	TAC AAT	GAT	CTG	ACC	AGG	CTG	ATT	GGC	AAC	TAC	ACC	GAT	TAC	GCT	GTG
245	624														
246	Tyr Asn	Asp	Leu	Thr	Arg	Leu	Ile	Gly	Asn	Tyr	Thr	Asp	Tyr	Ala	Val
247		195					200					205			
248															
249	CGC TGG	TAC	AAT	ACC	GGC	CTG	GAA	CGC	GTG	TGG	GGC	CCA	GAT	TCC	CGC
250	672														
251	Arg Trp	Tyr	Asn	Thr	Gly		Glu	Arg	Val	\mathtt{Trp}	_	Pro	Asp	Ser	Arg
252	210					215					220				
253															
254	GAT TGG	GTG	AGG	TAC	TAA	CAA	TTT	CGC	CGC	GAA	CTG	ACC	CTG	ACC	GTG
255	720														

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256 257	Asp Trp 225	Val	Arg	Tyr	Asn 230	Gln	Phe	Arg	Arg	Glu 235	Leu	Thr	Leu	Thr	Val 240
258 259 260	CTC GAT	ATC	GTG	GCT	CTG	TTC	CCA	AAT	TAC	GAT	AGC	CGC	CGC	TAC	CCA
261 262	Leu Asp	Ile	Val	Ala 245	Leu	Phe	Pro	Asn	Tyr 250	Asp	Ser	Arg	Arg	Tyr 255	Pro
263 264 265	ATT CGA 816	ACC	GTG	TCC	CAA	CTG	ACC	CGC	GAA	ATT	TAC	ACC	AAC	CCA	GTG
266 267 268	Ile Arg	Thr	Val 260	Ser	Gln	Leu	Thr	Arg 265	Glu	Ile	Tyr	Thr	Asn 270	Pro	Val
269 270	CTG GAA 864	AAT	TTT	GAT	GGT	AGC	TTT	CGC	GGC	TCC	GCT	CAG	GGC	ATC	GAA
271 272 273	Leu Glu	Asn 275	Phe	Asp	Gly	Ser	Phe 280	Arg	Gly	Ser	Ala	Gln 285	Gly	Ile	Glu
274 275	CGC AGC 912	ATT	AGG	AGC	CCA	CAT	CTG	ATG	GAT	ATC	CTG	AAC	AGC	ATC	ACC
276 277 278	Arg Ser 290	Ile	Arg	Ser	Pro	His 295	Leu	Met	Asp	Ile	Leu 300	Asn	Ser	Ile	Thr
279 280	ATC TAC 960	ACC	GAT	GCT	CAT	AGG	GGT	TAC	TAC	TAC	TGG	TCC	GGC	CAT	CAA
281 282 283	Ile Tyr 305	Thr	Asp	Ala	His 310	Arg	Gly	Tyr	Tyr	Tyr 315	Trp	Ser	Gly	His	Gln 320
284 285	ATC ATG 1008	GCT	TCC	CCT	GTG	GGC	TTT	TCC	GGG	CCA	GAA	TTC	ACC	TTT	CCA
286 287 288	Ile Met	Ala	Ser	Pro 325	Val	Gly	Phe	Ser	Gly 330	Pro	Glu	Phe	Thr	Phe 335	Pro
289 290	CTG TAC 1056														
291 292 293	Leu Tyr	Gly	Thr 340	Met	Gly	Asn	Ala	Ala 345	Pro	Gln	Gln	Arg	11e 350	Val	Ala
294 295	CAA CTG 1104														
296 297 298	Gln Leu	Gly 355	Gln	Gly	Val	Tyr	Arg 360	Thr	Leu	Ser	Ser	Thr 365	Leu	Tyr	Arg
299 300	CGC CCT 1152														
301 302 303	Arg Pro 370	Phe	Asn	Ile	Gly	Ile 375	Asn	Asn	Gln	Gln	Leu 380	Ser	Val	Leu	Asp
304 305	GGC ACC 1200														
306	Gly Thr	Glu	Phe	Ala	Tyr	Gly	Thr	Ser	Ser	Asn	Leu	Pro	Ser	Ala	Val

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307 308	385				390					395					400
309 310	TAC CGC 1248	AAG	AGC	GGC	ACC	GTG	GAT	TCC	CTG	GAT	GAA	ATC	CCA	CCA	CAG
311 312 313	Tyr Arg	Lys	Ser	Gly 405	Thr	Val	Asp	Ser	Leu 410	Asp	Glu	Ile	Pro	Pro 415	Gln
314 315	AAT AAC 1296	AAC	GTG	CCA	CCT	AGG	CAA	GGC	TTT	AGC	CAT	CGC	CTG	AGC	CAT
316 317 318	Asn Asn	Asn	Val 420	Pro	Pro	Arg	Gln	Gly 425	Phe	Ser	His	Arg	Leu 430	Ser	His
319 320	GTG TCC 1344	ATG	TTT	CGC	TCC	GGC	TTT	AGC	AAT	AGC	AGC	GTG	AGC	ATC	ATC
321 322 323	Val Ser	Met 435	Phe	Arg	Ser	Gly	Phe 440	Ser	Asn	Ser	Ser	Val 445	Ser	Ile	Ile
324 325	CGC GCT 1392	CCT	ATG	TTC	TCC	TGG	ATC	CAT	CGC	AGC	GCT	GAA	TTT	AAC	AAC
326 327 328	Arg Ala 450	Pro	Met	Phe	Ser	Trp 455	Ile	His	Arg	Ser	Ala 460	Glu	Phe	Asn	Asn
329 330	ATC ATT 1440	GCC	TCC	GAT	AGC	ATT	ACC	CAA	ATC	CCT	GCC	GTG	AAG	GGC	AAC
331 332 333	Ile Ile 465	Ala	Ser	Asp	Ser 470	Ile	Thr	Gln	Ile	Pro 475	Ala	Val	Lys	Gly	Asn 480
334 335	TTT CTG 1488	TTT	AAT	GGT	TCC	GTG	ATT	TCC	GGC	CCA	GGC	TTT	ACC	GGT	GGC
336 337 338	Phe Leu	Phe	Asn	Gly 485	Ser	Val	Ile	Ser	Gly 490	Pro	Gly	Phe	Thr	Gly 495	Gly
339 340	GAC CTG 1536	GTG	CGC	CTG	AAT	AGC	AGC	GGC	AAT	AAC	ATT	CAG	TAA	CGC	GGC
341 342 343	Asp Leu	Val	Arg 500	Leu	Asn	Ser	Ser	Gly 505	Asn	Asn	Ile	Gln	Asn 510	Arg	Gly
344 345	TAC ATT 1584	GAA	GTG	CCA	ATT	CAC	TTC	CCA	TCC	ACC	TCC	ACC	CGC	TAC	CGC
346 347 348	Tyr Ile	Glu 515	Val	Pro	Ile	His	Phe 520	Pro	Ser	Thr	Ser	Thr 525	Arg	Tyr	Arg
349 350	GTG CGC 1632	GTG	CGC	TAC	GCT	TCC	GTG	ACC	CCA	ATT	CAC	CTC	AAC	GTT	AAC
351 352 353	Val Arg 530	Val	Arg	Tyr	Ala	Ser 535	Val	Thr	Pro	Ile	His 540	Leu	Asn	Val	Asn
354 355	TGG GGC 1680	AAT	TCC	TCC	ATT	TTT	TCC	AAT	ACC	GTG	CCA	GCT	ACC	GCT	ACC
356 357	Trp Gly 545	Asn	Ser	Ser	Ile 550	Phe	Ser	Asn	Thr	Val 555	Pro	Ala	Thr	Ala	Thr 560

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358		ama	~~=		ama.	~~~			~-~							
359	TCC		GAT	AAT	CTG	CAA	TCC	AGC	GAT	TTT	GGT	TAC	TTT	GAA	AGC	GCC
360		28	•			~1		_	_	_,		_			_	
361	Ser	ьeu	Asp	Asn		GIN	ser	ser	Asp		GIY	Tyr	Pne	GIU		Ата
362					565					570					575	
363		~~		3.00	maa	maa	~=~	aam			~=~	~~=	~=~	~~~		
364	AAT		TTT	ACC	TCC	TCC	CTG	GGT	AAT.	ATC	GTG	GGT	GTG	CGC	AAT.	TTT
365	17		5 1	m1	.	_	_	~1	_			~1		_	_	-1
366	Asn .	Ата	Pne		ser	ser	ьeu	GIY		ile	vaı	GIA	vaı	_	Asn	Pne
367				580					585					590		
368	300	~~~		~~~	~~~	ст с			~~~	~~~		~~~		3 mm	~~~	~~~
369	AGC		ACC	GCC	GGC	GTG	ATC	ATC	GAC	CGC	J.I.I.	GAA	TTT	ATT.	CCA	GTG
370	18		em1		~3				_	_	-1	~7	51.	-1.		
371	Ser	GIY		Ата	GIY	vaı	тте		Asp	Arg	Pne	GIU		тте	Pro	vaı
372	•		595					600					605			
373	3.00	aaa	7.00	ama	a	ma a	1 m 7									
374	ACC		ACC	CTC	GAG	TAG	ďΑ									
375	18	_	m1	T	a1											
376	Thr .		Thr	Leu	GIU											
377		610														
378	(2)	TAIDO	\D\#\\		EOD	CEO	TD 1	70 . 1 1	1 .							
379	(2)	INFC	JRMAT	LTON	FOR	SEQ	ו עד	MO: T	L:							
380			/ .	יייטריי	2012	CITAT	י א מייים	an Tán	TOC.							
381		,	(1) 8	~	ENCE						_					
382 383				(A)	LEI	WGTH :	. PT	s am:	lno a	actas	3					
				(D)	CD3.27	NT			د :							
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384					TYI											
384 385		(2	: - \ x	(D)	TOI	POLOG	3Y:]	linea	ar							
384 385 386		i)	Li) N	(D)		POLOG	3Y:]	linea	ar							
384 385 386 387				(D)	TOLE	POLOC TYPI	3Y:] E: pi	linea	ar in	, to	NO. 1	11.				
384 385 386 387 388				(D)	TOI	POLOC TYPI	3Y:] E: pi	linea	ar in	O ID	NO: 1	11:				
384 385 386 387 388 389	Mot	()	ci) S	(D) MOLEC SEQUE	TOI CULE ENCE	TYPI DESC	SY: I S: pi	linea rotei rion:	ar in : SEÇ	•			Tree	ħ a n	Crea	Lou
384 385 386 387 388 389 390	Met .	()	ci) S	(D) MOLEC SEQUE	TOI CULE ENCE Pro	TYPI DESC	SY: I S: pi	linea rotei rion:	ar in : SEÇ	Cys			Tyr	Asn	_	Leu
384 385 386 387 388 389 390 391	Met .	()	ci) S	(D) MOLEC SEQUE	TOI CULE ENCE	TYPI DESC	SY: I S: pi	linea rotei rion:	ar in : SEÇ	•			Tyr	Asn	Cys 15	Leu
384 385 386 387 388 389 390 391 392	1	(x Asp	ci) S Asn	(D) MOLEC SEQUE Asn	TOI CULE ENCE Pro 5	POLOC TYPI DESC Asn	GY: 1 G: pi CRIPT	linea rotei rion: Asn	ar in : SEÇ Glu	Cys 10	Ile	Pro	_		15	
384 385 386 387 388 389 390 391 392 393		(x Asp	ci) S Asn	(D) MOLEC SEQUE Asn Glu	TOI CULE ENCE Pro 5	POLOC TYPI DESC Asn	GY: 1 G: pi CRIPT	linea rotei rion: Asn	ar in : SEÇ Glu Gly	Cys 10	Ile	Pro	_	Glu	15	
384 385 386 387 388 389 390 391 392 393 394	1	(x Asp	ci) S Asn	(D) MOLEC SEQUE Asn	TOI CULE ENCE Pro 5	POLOC TYPI DESC Asn	GY: 1 G: pi CRIPT	linea rotei rion: Asn	ar in : SEÇ Glu	Cys 10	Ile	Pro	_		15	
384 385 386 387 388 389 390 391 392 393 394 395	1 Ser	() Asp Asn	Asn Pro	(D) MOLEC SEQUE Asn Glu 20	TOPECULE ENCE Pro 5	TYPI DESC Asn Glu	E: pr CRIPT Ile Val	linea rotei rion: Asn Leu	in : SEÇ Glu Gly 25	Cys 10 Gly	Ile Glu	Pro Arg	Ile	Glu 30	15 Thr	Gly
384 385 386 387 388 389 390 391 392 393 394 395 396	1	() Asp Asn	Asn Pro	(D) MOLEC SEQUE Asn Glu 20	TOPECULE ENCE Pro 5	TYPI DESC Asn Glu	E: pr CRIPT Ile Val	linea cotei rion: Asn Leu Leu	in : SEÇ Glu Gly 25	Cys 10 Gly	Ile Glu	Pro Arg	Ile	Glu 30	15 Thr	Gly
384 385 386 387 388 390 391 392 393 394 395 396 397	1 Ser	() Asp Asn	Asn Pro	(D) MOLEC SEQUE Asn Glu 20	TOPECULE ENCE Pro 5	TYPI DESC Asn Glu	E: pr CRIPT Ile Val	linea rotei rion: Asn Leu	in : SEÇ Glu Gly 25	Cys 10 Gly	Ile Glu	Pro Arg	Ile	Glu 30	15 Thr	Gly
384 385 386 387 388 389 390 391 392 393 394 395 396 397 398	Ser Z	(> Asp Asn Thr	Asn Pro Pro 35	(D) MOLEG SEQUE Asn Glu 20 Ile	TOPECULE ENCE Pro 5 Val Asp	TYPE DESC Asn Glu	E: pr CRIPT Ile Val	rotei FION: Asn Leu Leu 40	in : SEÇ Glu Gly 25 Ser	Cys 10 Gly Leu	Ile Glu Thr	Pro Arg Gln	Ile Phe 45	Glu 30 Leu	15 Thr Leu	Gly Ser
384 385 386 387 388 390 391 392 393 394 395 396 397 398 399	1 Ser	(>Asp Asn Thr	Asn Pro Pro 35	(D) MOLEG SEQUE Asn Glu 20 Ile	TOPECULE ENCE Pro 5 Val Asp	TYPE DESC Asn Glu	E: processor pro	rotei FION: Asn Leu Leu 40	in : SEÇ Glu Gly 25 Ser	Cys 10 Gly Leu	Ile Glu Thr	Pro Arg Gln Leu	Ile Phe 45	Glu 30 Leu	15 Thr Leu	Gly Ser
384 385 386 387 388 390 391 392 393 394 395 396 397 398 399 400	Ser Z	(> Asp Asn Thr	Asn Pro Pro 35	(D) MOLEG SEQUE Asn Glu 20 Ile	TOPECULE ENCE Pro 5 Val Asp	TYPE DESC Asn Glu	E: pr CRIPT Ile Val	rotei FION: Asn Leu Leu 40	in : SEÇ Glu Gly 25 Ser	Cys 10 Gly Leu	Ile Glu Thr	Pro Arg Gln	Ile Phe 45	Glu 30 Leu	15 Thr Leu	Gly Ser
384 385 386 387 388 390 391 392 393 394 395 396 397 398 399 400 401	Ser A	(xAsp Asn Thr Phe 50	Asn Pro Pro 35	(D) MOLEG SEQUE Asn Glu 20 Ile	TON CULE ENCE Pro 5 Val Asp	TYPE DESC Asn Glu Ile	E: processor pro	rotei FION: Asn Leu Leu 40 Phe	in : SEG Glu Gly 25 Ser Val	Cys 10 Gly Leu	Ile Glu Thr	Pro Arg Gln Leu 60	Ile Phe 45	Glu 30 Leu Asp	15 Thr Leu Ile	Gly Ser Ile
384 385 386 387 388 390 391 392 393 394 395 396 397 398 399 400 401 402	Ser Tyr Glu	(xAsp Asn Thr Phe 50	Asn Pro Pro 35	(D) MOLEG SEQUE Asn Glu 20 Ile	TON CULE ENCE Pro 5 Val Asp	TYPE DESC Asn Glu Ile Ala	E: processor pro	rotei FION: Asn Leu Leu 40 Phe	in : SEG Glu Gly 25 Ser Val	Cys 10 Gly Leu	Ile Glu Thr Gly Ala	Pro Arg Gln Leu 60	Ile Phe 45	Glu 30 Leu Asp	15 Thr Leu Ile	Gly Ser Ile
384 385 386 387 388 390 391 392 393 394 395 396 397 398 399 400 401 402 403	Ser A	(xAsp Asn Thr Phe 50	Asn Pro Pro 35	(D) MOLEG SEQUE Asn Glu 20 Ile	TON CULE ENCE Pro 5 Val Asp	TYPE DESC Asn Glu Ile	E: processor pro	rotei FION: Asn Leu Leu 40 Phe	in : SEG Glu Gly 25 Ser Val	Cys 10 Gly Leu	Ile Glu Thr	Pro Arg Gln Leu 60	Ile Phe 45	Glu 30 Leu Asp	15 Thr Leu Ile	Gly Ser Ile
384 385 386 387 388 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404	Ser A	(>Asp Asn Thr Phe 50	Asn Pro Pro 35 Val	(D) MOLEG SEQUE Asn Glu 20 Ile Pro	TON CULE ENCE Pro 5 Val Asp Gly	TYPE DESC Asn Glu Ile Ala Pro	E: processor pro	rotei FION: Asn Leu 40 Phe	in SEG Glu Gly 25 Ser Val	Cys 10 Gly Leu Leu	Ile Glu Thr Gly Ala 75	Pro Arg Gln Leu 60 Phe	Ile Phe 45 Val Leu	Glu 30 Leu Asp	15 Thr Leu Ile Gln	Gly Ser Ile Ile 80
384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405	Ser Tyr Glu	(>Asp Asn Thr Phe 50	Asn Pro Pro 35 Val	(D) MOLEG SEQUE Asn Glu 20 Ile Pro	TONEULE Pro 5 Val Asp Gly Asn	TYPE DESC Asn Glu Ile Ala Pro	E: processor pro	rotei FION: Asn Leu 40 Phe	in SEG Glu Gly 25 Ser Val	Cys 10 Gly Leu Leu Asp	Ile Glu Thr Gly Ala 75	Pro Arg Gln Leu 60 Phe	Ile Phe 45 Val Leu	Glu 30 Leu Asp	15 Thr Leu Ile Gln	Gly Ser Ile Ile 80
384 385 386 387 388 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406	Ser A	(>Asp Asn Thr Phe 50	Asn Pro Pro 35 Val	(D) MOLEG SEQUE Asn Glu 20 Ile Pro	TON CULE ENCE Pro 5 Val Asp Gly	TYPE DESC Asn Glu Ile Ala Pro	E: processor pro	rotei FION: Asn Leu 40 Phe	in SEG Glu Gly 25 Ser Val	Cys 10 Gly Leu Leu	Ile Glu Thr Gly Ala 75	Pro Arg Gln Leu 60 Phe	Ile Phe 45 Val Leu	Glu 30 Leu Asp	15 Thr Leu Ile Gln	Gly Ser Ile Ile 80
384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405	Ser A	(>Asp Asn Thr Phe 50 Gly	Asn Pro Pro 35 Val Ile Leu	(D) MOLEG SEQUE Asn Glu 20 Ile Pro Phe Ile	TONECULE Pro 5 Val Asp Gly Gly Asn 85	TYPE DESC Asn Glu Ile Ala Pro 70 Gln	E: processor pro	Cotes FION: Asn Leu 40 Phe Gln Ile	in SEG Glu Gly 25 Ser Val Trp Glu	Cys 10 Gly Leu Leu Asp Glu 90	Ile Glu Thr Gly Ala 75 Phe	Pro Arg Gln Leu 60 Phe	Ile Phe 45 Val Leu Arg	Glu 30 Leu Asp Val	15 Thr Leu Ile Gln Gln 95	Gly Ser Ile Ile 80 Ala

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409				100					105					110		
410 411 412	Ser	Phe	Arg 115	Glu	Trp	Glu	Ala	Asp 120	Pro	Thr	Asn	Pro	Ala 125	Leu	Arg	Glu
413 414 415	Glu	Met 130	Arg	Ile	Gln	Phe	Asn 135	Asp	Met	Asn	Ser	Ala 140	Leu	Thr	Thr	Ala
416 417 418 419	Ile 145	Pro	Leu	Phe	Ala	Val 150	Gln	Asn	Tyr	Gln	Val 155	Pro	Leu	Leu	Ser	Val 160
420 421 422	Tyr	Val	Gln	Ala	Ala 165	Asn	Leu	His	Leu	Ser 170	Val	Leu	Arg	Asp	Val 175	Ser
423 424 425	Val	Phe	Gly	Gln 180	Arg	Trp	Gly	Phe	Asp 185	Ala	Ala	Thr	Ile	Asn 190	Ser	Arg
426 427 428	Tyr	Asn	Asp 195	Leu	Thr	Arg	Leu	Ile 200	Gly	Asn	Tyr	Thr	Asp 205	Tyr	Ala	Val
429 430 431	Arg	Trp 210	Tyr	Asn	Thr	Gly	Leu 215	Glu	Arg	Val	Trp	Gly 220	Pro	Asp	Ser	Arg
432 433 434	Asp 225	Trp	Val	Arg	Tyr	Asn 230	Gln	Phe	Arg	Arg	Glu 235	Leu	Thr	Leu	Thr	Val 240
435 436 437	Leu	Asp	Ile	Val	Ala 245	Leu	Phe	Pro	Asn	Tyr 250	Asp	Ser	Arg	Arg	Tyr 255	Pro
438 439 440	Ile	Arg	Thr	Val 260	Ser	Gln	Leu	Thr	Arg 265	Glu	Ile	Tyr	Thr	Asn 270	Pro	Val
441 442 443	Leu	Glu	Asn 275	Phe	Asp	Gly	Ser	Phe 280	Arg	Gly	Ser	Ala	Gln 285	Gly	Ile	Glu
444 445 446	Arg	Ser 290	Ile	Arg	Ser	Pro	His 295	Leu	Met	Asp	Ile	Leu 300	Asn	Ser	Ile	Thr
447 448 449	Ile 305	Tyr	Thr	Asp	Ala	His 310	Arg	Gly	Tyr	Tyr	Tyr 315	Trp	Ser	Gly	His	Gln 320
450 451 452	Ile	Met	Ala	Ser	Pro 325	Val	Gly	Phe	Ser	Gly 330	Pro	Glu	Phe	Thr	Phe 335	Pro
453 454 455	Leu	Tyr	Gly	Thr 340	Met	Gly	Asn	Ala	Ala 345	Pro	Gln	Gln	Arg	Ile 350	Val	Ala
456 457 458	Gln	Leu	Gly 355	Gln	Gly	Val	Tyr	Arg 360	Thr	Leu	Ser	Ser	Thr 365	Leu	Tyr	Arg
459	Arg	Pro	Phe	Asn	Ile	Gly	Ile	Asn	Asn	Gln	Gln	Leu	Ser	Val	Leu	Asp

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460 461		370					375					380				
462 463 464	Gly 385	Thr	Glu	Phe	Ala	Tyr 390	Gly	Thr	Ser	Ser	Asn 395	Leu	Pro	Ser	Ala	Val 400
465 466 467	Tyr	Arg	Lys	Ser	Gly 405	Thr	Val	Asp	Ser	Leu 410	Asp	Glu	Ile	Pro	Pro 415	Gln
468 469 470	Asn	Asn	Asn	Val 420	Pro	Pro	Arg	Gln	Gly 425	Phe	Ser	His	Arg	Leu 430	Ser	His
471 472 473	Val	Ser	Met 435	Phe	Arg	Ser	Gly	Phe 440	Ser	Asn	Ser	Ser	Val 445	Ser	Ile	Ile
474 475 476	Arg	Ala 450	Pro	Met	Phe	Ser	Trp 455	Ile	His	Arg	Ser	Ala 460	Glu	Phe	Asn	Asn
477 478 479	Ile 465	Ile	Ala	Ser	Asp	Ser 470	Ile	Thr	Gln	Ile	Pro 475	Ala	Val	Lys	Gly	Asn 480
480 481 482	Phe	Leu	Phe	Asn	Gly 485	Ser	Val	Ile	Ser	Gly 490	Pro	Gly	Phe	Thr	Gly 495	Gly
483 484 485	Asp	Leu	Val	Arg 500	Leu	Asn	Ser	Ser	Gly 505	Asn	Asn	Ile	Gln	Asn 510	Arg	Gly
486 487 488	Tyr	Ile	Glu 515	Val	Pro	Ile	His	Phe 520	Pro	Ser	Thr	Ser	Thr 525	Arg	Tyr	Arg
489 490 491	Val	Arg 530	Val	Arg	Tyr	Ala	Ser 535	Val	Thr	Pro	Ile	His 540	Leu	Asn	Val	Asn
492 493 494	Trp 545	Gly	Asn	Ser	Ser	Ile 550	Phe	Ser	Asn	Thr	Val 555	Pro	Ala	Thr	Ala	Thr 560
495 496 497	Ser	Leu	Asp	Asn	Leu 565	Gln	Ser	Ser	Asp	Phe 570	Gly	Tyr	Phe	Glu	Ser 575	Ala
498 499 500	Asn	Ala	Phe	Thr 580	Ser	Ser	Leu	Gly	Asn 585	Ile	Val	Gly	Val	Arg 590	Asn	Phe
501 502 503	Ser	Gly	Thr 595	Ala	Gly	Val	Ile	Ile 600	Asp	Arg	Phe	Glu	Phe 605	Ile	Pro	Val
504 505 506	Thr	Ala 610	Thr	Leu	Glu											
507 508 509	(2)				FOR											
510					ENGTI					rs						

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511 512 513 514	(B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic)														
515 516	(ii) MO	LECU	LE T	YPE:	DNA	(gei	nomi	2)						
517 518	(ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 11842														
519 520	(A) NAME/KEY: CDS														
521 522	(xi) SE	QUEN	CE DI	ESCR:	IPTI	ON:	SEQ :	ID NO	0:12	:				
523 524	ATG GAT	AAC	AAT	CCG	AAC	ATC	AAT	GAA	TGC	ATT	CCT	TAC	AAT	TGC	CTC
525 526 527	Met Asp	Asn	Asn	Pro 5	Asn	Ile	Asn	Glu	Cys 10	Ile	Pro	Tyr	Asn	Cys 15	Leu
528 529	AGC AAC	CCT	GAA	GTG	GAA	GTG	CTG	GGT	GGC	GAA	CGC	ATC	GAA	ACC	GGT
530 531 532	Ser Asn	Pro	Glu 20	Val	Glu	Val	Leu	Gly 25	Gly	Glu	Arg	Ile	Glu 30	Thr	Gly
533 534	TAC ACC	CCA	ATC	GAT	ATT	TCC	CTG	TCC	CTG	ACC	CAA	TTT	CTG	CTG	AGC
535 536 537	Tyr Thr	Pro 35	Ile	Asp	Ile	Ser	Leu 40	Ser	Leu	Thr	Gln	Phe 45	Leu	Leu	Ser
538 539	GAA TTT 192	GTG	CCC	GGT	GCT	GGC	TTT	GTG	CTG	GGC	CTG	GTG	GAT	ATC	ATC
540 541 542	Glu Phe 50	Val	Pro	Gly	Ala	Gly 55	Phe	Val	Leu	Gly	Leu 60	Val	Asp	Ile	Ile
543 544	TGG GGC 240	ATT	TTT	GGT	CCC	TCC	CAA	TGG	GAC	GCC	TTT	CTG	GTG	CAA	ATT
545 546 547	Trp Gly 65	Ile	Phe	Gly	Pro 70	Ser	Gln	Trp	Asp	Ala 75	Phe	Leu	Val	Gln	Ile 80
548 549	GAA CAG 288	CTG	ATT	AAC	CAA	CGC	ATC	GAA	GAA	TTC	GCT	AGG	AAC	CAA	GCC
550 551 552	Glu Gln	Leu	Ile	Asn 85	Gln	Arg	Ile	Glu	Glu 90	Phe	Ala	Arg	Asn	Gln 95	Ala
553 554	ATT TCC 336	CGC	CTG	GAA	GGC	CTG	AGC	AAT	CTG	TAC	CAA	ATT	TAC	GCC	GAA
555 556 557	Ile Ser	Arg	Leu 100	Glu	Gly	Leu	Ser	Asn 105	Leu	Tyr	Gln	Ile	Tyr 110	Ala	Glu
558 559	TCC TTT	CGC	GAG	TGG	GAA	GCC	GAT	CCT	ACC	AAT	CCA	GCC	CTG	CGC	GAA
560 561	Ser Phe	Arg 115	Glu	Trp	Glu	Ala	Asp 120	Pro	Thr	Asn	Pro	Ala 125	Leu	Arg	Glu

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562															
563	GAG ATG	CGC	ATT	CAA	TTC	AAT	GAC	ATG	AAC	AGC	GCC	CTG	ACC	ACC	GCT
564	432														
565	Glu Met	Arg	Ile	Gln	Phe	Asn	Asp	Met	Asn	Ser	Ala	Leu	Thr	Thr	Ala
566	130					135					140				
567	·														
568	ATT CCT	CTG	TTT	GCC	GTG	CAA	AAT	TAC	CAA	GTG	CCT	CTG	CTG	TCC	GTG
569	480	7	Dl	31-	*** 7	a 1	•	m	a 1 .	••• •	5		. .		
570 571	Ile Pro	ьeu	Pne	Ата		GIN	Asn	Tyr	GIN		Pro	ьeu	ьeu	ser	
571 572	145				150					155					160
573	TAC GTG	ממי	ССТ	פרר	דע ע	СТС	СУТ	СТС	דרר	стс	СТС	CGC	СУТ	стс	TCC
574	528	Crus	001	000	mi	CIO	CAI	CIG	100	010	010	CGC	OAI	010	100
575	Tyr Val	Gln	Ala	Ala	Asn	Leu	His	Leu	Ser	Val	Leu	Arg	Asp	Val	Ser
576	-1-			165					170			5		175	
577															
578	GTG TTT	GGC	CAA	AGG	TGG	GGC	TTT	GAT	GCC	GCC	ACC	ATC	AAT	AGC	CGC
579	576														
580	Val Phe	Gly	Gln	Arg	Trp	Gly	Phe	Asp	Ala	Ala	Thr	Ile	Asn	Ser	Arg
581			180					185					190		
582															
583	TAC AAT	GAT	CTG	ACC	AGG	CTG	ATT	GGC	AAC	TAC	ACC	GAT	TAC	GCT	GTG
584	624	7	.	ml	3	T	- 1.	a 1	3		ml	7	m	77-	17-7
585	Tyr Asn	_	ьeu	Thr	Arg	ьeu		GTA	Asn	Tyr	Thr	_	Tyr	Ата	vaı
586 587		195					200					205			
588	CGC TGG	ТΔС	דע ע	ΔCC	GGC	СТС	GDD	CGC	стс	тсс	GGC	$CC\Delta$	СΣΤ	тсс	CGC
589	672	1110	***	1100	-	010	01111		010	100	000		0.11	100	
590	Arg Trp	Tvr	Asn	Thr	Glv	Leu	Glu	Ara	Val	Trp	Glv	Pro	Asp	Ser	Ara
591	210	- 2 -			4	215		5			220				3
592															
593	GAT TGG	GTG	AGG	TAC	AAT	CAA	TTT	CGC	CGC	GAA	CTG	ACC	CTG	ACC	GTG
594	720														
595	Asp Trp	Val	Arg	Tyr		Gln	Phe	Arg	Arg		Leu	Thr	Leu	Thr	
596	225				230					235					240
597	CMC CAM	3 m.a	ama	aam	ama	mma	aa	3 3 m	m* a	~ m	7.00	999	a aa	ma a	aa3
598 599	CTC GAT	ATC	GTG	GCT	CTG	TTC	CCA	AAT	TAC	GAT	AGC	CGC	CGC	TAC	CCA
600	Leu Asp	т1д	V=1	λla	T.211	Dhe	Dro	λen	ጥኒታ	Man	Sar	Ara	Ara	ጥኒፖ	Pro
601	neu Asp	116	vai	245	пец	FIIC	FIO	ASII	250	дор	Der	Arg	Arg	255	110
602				217					250					233	
603	ATT CGA	ACC	GTG	TCC	CAA	CTG	ACC	CGC	GAA	ATT	TAC	ACC	AAC	CCA	GTG
604	816												= ='		· -
605	Ile Arg	Thr	Val	Ser	Gln	Leu	Thr	Arg	Glu	Ile	Tyr	Thr	Asn	Pro	Val
606	•		260					265			-		270		
607															
608	CTG GAA	AAT	TTT	GAT	GGT	AGC	TTT	CGC	GGC	TCC	GCT	CAG	GGC	ATC	GAA
609	864	_		_		_	_,	_		_					~-7
610	Leu Glu		Phe	Asp	GTA	Ser		Arg	Gly	Ser	Ala		GIY	Ile	GIu
611		275					280					285			
612															

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613	CGC AGC	ATT	AGG	AGC	CCA	CAT	CTG	ATG	GAT	ATC	CTG	AAC	AGC	ATC	ACC
614	912														
· 615	Arg Ser	Ile	Arg	Ser	Pro	His	Leu	Met	Asp	Ile	Leu	Asn	Ser	Ile	Thr
616	290					295					300				
617															
618	ATC TAC	ACC	GAT	GCT	CAT	AGG	GGT	TAC	TAC	TAC	TGG	TCC	GGC	CAT	CAA
619	960	mb so	7 ~~	7 T -	774 ~	7	01	Ma				C	a 1	TT-1	~1
620 621	Ile Tyr	Thr	Asp	Ala	310	arg	GIY	Tyr	ıyr	1yr 315	Trp	ser	GIA	HIS	
622	305				210					313					320
623	ATC ATG	CCT	TCC	ССТ	стс	GGC	ттт	ጥሮሮ	GGG	CCA	CDD	ጥጥር	ΔCC	արարար	CCA
624	1008	GCI	100	CCI	010	000	111	100	000	CCA	OAA	110	ACC	111	CCA
625	Ile Met	Ala	Ser	Pro	Val	Glv	Phe	Ser	Glv	Pro	Glu	Phe	Thr	Phe	Pro
626				325		1			330					335	
627															
628	CTG TAC	GGC	ACG	ATG	GGC	AAT	GCC	GCT	CCA	CAA	CAA	CGC	ATT	GTG	GCT
629	1056														
630	Leu Tyr	Gly	Thr	Met	Gly	Asn	Ala	Ala	Pro	Gln	Gln	Arg	Ile	Val	Ala
631			340					345					350		
632															
633	CAA CTG	GGT	CAG	GGC	GTG	TAC	CGC	ACC	CTG	TCC	TCC	ACC	CTG	TAC	CGC
634	1104					_	_		_	_	_		_	_	_
635	Gln Leu	_	Gln	GLY	Val	Tyr	_	Thr	Leu	Ser	Ser		Leu	Tyr	Arg
636		355					360					365			
637 638	CGC CCT	mmm.	יייאר	איזייט	ccc	አ ጥ <i>ር</i> '	አአሮ	7 7 C	CAC	~ A A	CTC	TOO	CTC	CTC	CAC
639	1152	111	AAI	AIC	GGC	AIC	AAC	AAC	CAG	CAA	CIG	100	GIG	CIG	GAC
640	Arg Pro	Phe	Δsn	Tle	Glv	Tle	Δsn	Agn	Gln	Gln	Leu	Ser	Val	T.en	Asn
641	370		11011		Q - 7	375	11011	11011	Q	0111	380				1101
642	3,0					0.0									
643	GGC ACC	GAA	TTT	GCT	TAC	GGC	ACC	TCC	TCC	AAT	CTG	CCA	TCC	GCT	GTA
644	1200														
645	Gly Thr	Glu	Phe	Ala	Tyr	Gly	Thr	Ser	Ser	Asn	Leu	${\tt Pro}$	Ser	Ala	Val
646	385				390					395					400
647															
648	TAC CGC	AAG	AGC	GGC	ACC	GTG	GAT	TCC	CTG	GAT	GAA	ATC	CCA	CCA	CAG
649	1248	_	_		_,		_	_	_	_	~-7		_	_	~-3
650	Tyr Arg	Lys	Ser	-	Thr	Val	Asp	Ser		Asp	GIU	IIe	Pro		GIn
651				405					410					415	
652 653	AAT AAC	አአሮ	CTC	CCA	CCT	N.C.C.	C 7 7	ccc	т	אככ	ርአጥ	ccc	СТС	אפפ	ርስጥ
654	1296	AAC	GIG	CCA	CCI	AGG	CAA	GGC	111	AGC	CAI	CGC	CIG	AGC	CAI
655	Asn Asn	Asn	Val	Pro	Pro	Ara	Gln	Glv	Phe	Ser	His	Ara	T.eu	Ser	His
656			420			5		425				9	430		
657															
658	GTG TCC	ATG	TTT	CGC	TCC	GGC	TTT	AGC	AAT	AGC	AGC	GTG	AGC	ATC	ATC
659	1344														
660	Val Ser	Met	Phe	Arg	Ser	Gly	Phe	Ser	Asn	Ser	Ser	Val	Ser	Ile	Ile
661		435					440					445			
662															
663	CGC GCT	CCT	ATG	TTC	TCC	TGG	ATC	CAC	CGC	TCC	GCT	GAG	TTC	AAC	AAC

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664	1392														
665	Arg Ala	Pro	Met	Phe	Ser	Trp	Ile	His	Arg	Ser	Ala	Glu	Phe	Asn	Asn
666	450					455			_		460				
667															
668	ATC ATC	CCG	TCC	TCC	CAA	ATC	ACC	CAA	ATC	CCG	CTC	ACC	AAG	TCC	ACG
669	1440														
670	Ile Ile	Pro	Ser	Ser		Ile	Thr	Gln	Ile	Pro	Leu	Thr	Lys	Ser	Thr
671	465				470					475					480
672															
673	AAC CTC	GGC	TCC	GGC	ACG	TCC	GTC	GTC	AAG	GGC	CCG	GGC	TTC	ACC	GGC
674	1488		_	~		_			_		_				
675	Asn Leu	GIY	Ser		Thr	Ser	Val	Val		GIY	Pro	GIY	Phe		GIA
676				485					490					495	
677	000 070	3.00	ama	000	000	3.00	maa	999	~~~	a	3 ma	maa	3.00	ama	aaa
678 679	GGC GAC 1536	ATC	CTC	CGC	CGC	ACG	TCC	CCG	GGC	CAG	ATC	TCC	ACC	CTC	CGC
680	Gly Asp	т1.	T 011	7.~~	7~~	Thr	cor	Dro	C111	Cln	т1 о	cor	Thr	Tou	7.20
681	GIY ASP	116	500	AIG	Arg	1111	Ser	505	СТУ	GIII	TTE	261	510	neu	Arg
682			300					303					310		
683	GTC AAC	ΔΤΟ	ΔCG	ССТ	CCG	СТС	AGC	CAG	CGC	TAC	AGG	GTG	CGC	ΔΤΟ	AGA
684	1584		1100	001				C110		1110	1100	010			
685	Val Asn	Ile	Thr	Ala	Pro	Leu	Ser	Gln	Ara	Tvr	Ara	Val	Ara	Ile	Ara
686		515					520		5	-1-	3	525	5		3
687															
688	TAC GCT	AGC	ACG	ACC	AAC	CTG	CAA	TTC	CAC	ACG	TCC	ATC	GAC	GGC	AGA
689	1632														
690	Tyr Ala	Ser	Thr	Thr	Asn	Leu	Gln	Phe	His	Thr	Ser	Ile	Asp	Gly	Arg
691	530					535					540		_	_	_
692															
693	CCG ATC	AAC	CAG	GGC	AAC	TTC	AGC	GCG	ACG	ATG	AGC	TCC	GGG	TCC	AAC
694	1680														
695	Pro Ile	Asn	Gln	Gly	Asn	Phe	Ser	Ala	Thr	Met	Ser	Ser	Gly	Ser	Asn
696	545				550					555					560
697															
698	CTC CAG	TCC	GGC	TCC	TTC	CGC	ACG	GTC	GGT	TTC	ACC	ACG	CCG	TTC	AAC
699	1728														_
700	Leu Gln	Ser	Gly		Phe	Arg	Thr	Val	-	Phe	Thr	Thr	Pro		Asn
701				565					570					575	
702	mma maa	330	~~~	maa	maa	ama	mma	3.00	ama	maa	aam	a	ama	mma	220
703	TTC TCC	AAC	GGC	TCC	TÇÇ	GTC	TTC	ACG	CTC	TCC	GCT	CAC	GTC	TTC	AAC
704 705	1776	7 ~~	<u>ما</u>	Com	Com	1707	Dho	Th.	T 011	C 0 70	77-	Hic	1707	Dho	7 an
705 706	Phe Ser	ASII	580	ser	ser	Val	Pne	585	Leu	ser	Ala	птэ	590	Pne	ASII
707			300					565					390		
707	TCC GGC	מממ	GAG	стс	ግልጥ	ΔΤΟ	GAC	רפר	ΔͲሮ	GAG	ጥጥር	GTC	ררפ	GCC	GAG
709	1824	AAC	UAU	010	170	AIC	O.A.C			CAU	110	010			0.10
710	Ser Gly	Asn	Glu	Val	Tvr	Ile	Asp	Ara	Ile	Glu	Phe	Val	Pro	Ala	Glu
711	301 01y	595			-1-		600	3				605			
712															
713	GTC ACC	TTC	GAG	CTC	GAG	TAG	STA								
714	1848														

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715 716 717	Val	Thr 610	Phe	Glu	Leu	Glu										
718 719	(2)	INF	ORMA'	rion	FOR	SEQ	ID 1	NO:1	3:							
720 721			(i) s	SEQUI	ENCE	CHAI	RACTI	ERIS'	rics	:						
722									ino a	acids	3					
723 724						?E: a										
725				(D)	101	POLO	31 ; .	rriie	1 1							
726 727		(:	ii) N	MOLE	CULE	TYPE	E: p	rote:	in							
728 729		(:	xi) S	SEQUI	ENCE	DESC	CRIP	rion	: SE(Q ID	NO:	13:				
730	Met	Asp	Asn	Asn	Pro	Asn	Ile	Asn	Glu	Cys	Ile	Pro	Tyr	Asn	Cys	Leu
731	1				5					10					15	
732 733	Sar	λan	Pro	Glu	Ual	Gl 11	Wa l	Len	Glv	Gl _W	Glu	λνα	Tla	Glu	Thr	Gl v
734	261	ASII	PIO	20	vai	GIU	vai	пец	25	Gry	GIU	лгg	116	30	1111	GIY
735																
736	Tyr	Thr	Pro	Ile	Asp	Ile	Ser		Ser	Leu	Thr	Gln		Leu	Leu	Ser
737			35					40					45			
738 739	Glu	Dhe	Val	Pro	Glv	Δla	Glv	Dhe	Val	I.e.i	Glv	T.e.ii	Val	Δsn	Tle	Tle
740	014	50	var	110	O _T y	7114	55	1110	Vu	ДСЦ	- 1	60	Vul	тор		
741																
742	_	Gly	Ile	Phe	Gly	Pro	Ser	Gln	${\tt Trp}$	Asp	Ala	Phe	Leu	Val	Gln	
743	65					70					75					80
744 745	Glu	Gln	Leu	Tle	Asn	Gln	Ara	Tle	Glu	Glu	Phe	Δla	Ara	Asn	Gln	Ala
746	0_0	0111			85	0				90			5	-1011	95	
747																
748	Ile	Ser	Arg		Glu	Gly	Leu	Ser		Leu	Tyr	Gln	Ile	-	Ala	Glu
749 750				100					105					110		
751	Ser	Phe	Arq	Glu	Trp	Glu	Ala	Asp	Pro	Thr	Asn	Pro	Ala	Leu	Arq	Glu
752			115		_			120					125		J	
753				_	_	_								_		
754	Glu		Arg	Ile	Gln	Phe							Leu	Thr	Thr	Ala
755 756		130					133					140				
757	Ile	Pro	Leu	Phe	Ala	Val	Gln	Asn	Tyr	Gln	Val	Pro	Leu	Leu	Ser	Val
758	145					150			•		155					160
759	_					_	_		_	_		_	_	_		_
760 761	Tyr	val	Gln	Ala	Ala 165	Asn	ьeu	Hıs	Leu	Ser 170	val	ьeu	Arg	Asp	Val 175	ser
761 762					100					1/0					1/3	
763	Val	Phe	Gly	Gln	Arg	Trp	Gly	Phe	Asp	Ala	Ala	Thr	Ile	Asn	Ser	Arg
764				180					185					190		
765																

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766 767 768	Tyr	Asn	Asp 195	Leu	Thr	Arg	Leu	Ile 200	Gly	Asn	Tyr	Thr	Asp 205	Tyr	Ala	Val
769 770 771	Arg	Trp 210	Tyr	Asn	Thr	Gly	Leu 215	Glu	Arg	Val	Trp	Gly 220	Pro	Asp	Ser	Arg
772 773 774	Asp 225	Trp	Val	Arg	Tyr	Asn 230	Gln	Phe	Arg	Arg	Glu 235	Leu	Thr	Leu	Thr	Val 240
775 776 777	Leu	Asp	Ile	Val	Ala 245	Leu	Phe	Pro	Asn	Tyr 250	Asp	Ser	Arg	Arg	Tyr 255	Pro
778 779 780	Ile	Arg	Thr	Val 260	Ser	Gln	Leu	Thr	Arg 265	Glu	Ile	Tyr	Thr	Asn 270	Pro	Val
781 782 783	Leu	Glu	Asn 275	Phe	Asp	Gly	Ser	Phe 280	Arg	Gly	Ser	Ala	Gln 285	Gly	Ile	Glu
784 785 786	Arg	Ser 290	Ile	Arg	Ser	Pro	His 295	Leu	Met	Asp	Ile	Leu 300	Asn	Ser	Ile	Thr
787 788 789	Ile 305	Tyr	Thr	Asp	Ala	His 310	Arg	Gly	Tyr	Tyr	Tyr 315	Trp	Ser	Gly	His	Gln 320
790 791 792	Ile	Met	Ala	Ser	Pro 325	Val	Gly	Phe	Ser	Gly 330	Pro	Glu	Phe	Thr	Phe 335	Pro
793 794 795	Leu	Tyr	Gly	Thr 340	Met	Gly	Asn	Ala	Ala 345	Pro	Gln	Gln	Arg	Ile 350	Val	Ala
796 797 798	Gln	Leu	Gly 355	Gln	Gly	Val	Tyr	Arg 360	Thr	Leu	Ser	Ser	Thr 365	Leu	Tyr	Arg
799 800 801	Arg	Pro 370	Phe	Asn	Ile	Gly	Ile 375	Asn	Asn	Gln	Gln	Leu 380	Ser	Val	Leu	Asp
802 803 804	Gly 385	Thr	Glu	Phe	Ala	Tyr 390	Gly	Thr	Ser	Ser	Asn 395	Leu	Pro	Ser	Ala	Val 400
805 806 807	Tyr	Arg	Lys	Ser	Gly 405	Thr	Val	Asp	Ser	Leu 410	Asp	Glu	Ile	Pro	Pro 415	Gln
808 809 810	Asn	Asn	Asn	Val 420	Pro	Pro	Arg	Gln	Gly 425	Phe	Ser	His	Arg	Leu 430	Ser	His
811 812 813	Val	Ser	Met 435	Phe	Arg	Ser	Gly	Phe 440	Ser	Asn	Ser	Ser	Val 445	Ser	Ile	Ile
814 815 816	Arg	Ala 450	Pro	Met	Phe	Ser	Trp 455	Ile	His	Arg	Ser	Ala 460	Glu	Phe	Asn	Asn

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817 818 819	Ile 465	Ile	Pro	Ser	Ser	Gln 470	Ile	Thr	Gln	Ile	Pro 475	Leu	Thr	Lys	Ser	Thr 480
820 821 822	Asn	Leu	Gly	Ser	Gly 485	Thr	Ser	Val	Val	Lys 490	Gly	Pro	Gly	Phe	Thr 495	Gly
823 824 825	Gly	Asp	Ile	Leu 500	Arg	Arg	Thr	Ser	Pro 505	Gly	Gln	Ile	Ser	Thr 510	Leu	Arg
826 827 828	Val	Asn	Ile 515	Thr	Ala	Pro	Leu	Ser 520	Gln	Arg	Tyr	Arg	Val 525	Arg	Ile	Arg
829 830 831	Tyr	Ala 530	Ser	Thr	Thr	Asn	Leu 535	Gln	Phe	His	Thr	Ser 540	Ile	Asp	Gly	Arg
832 833 834	Pro 545	Ile	Asn	Gln	Gly	Asn 550	Phe	Ser	Ala	Thr	Met 555	Ser	Ser	Gly	Ser	Asn 560
835 836 837	Leu	Gln	Ser	Gly	Ser 565	Phe	Arg	Thr	Val	Gly 570	Phe	Thr	Thr	Pro	Phe 575	Asn
838 839 840	Phe	Ser	Asn	Gly 580	Ser	Ser	Val	Phe	Thr 585	Leu	Ser	Ala	His	Val 590	Phe	Asn
841 842 843	Ser	Gly	Asn 595	Glu	Val	Tyr	Ile	Asp 600	Arg	Ile	Glu	Phe	Val 605	Pro	Ala	Glu
844 845 846	Val	Thr 610	Phe	Glu	Leu	Glu										

SEQUENCE VERIFICATION REPORT PATENT APPLICATION US/08/113,561

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Line	Error	Original Text
28	Wrong application Serial Number	(A) APPLICATION NUMBER: unknown
29	Wrong Filing Date	(B) FILING DATE: August 25, 1993
30	Wrong Classification	(C) CLASSIFICATION: unknown
78	Entered (29) and Calc. Seq. Length (0) differ	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
92 ·	Entered (29) and Calc. Seq. Length (0) differ	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
106	Entered (49) and Calc. Seq. Length (0) differ	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
120	Entered (49) and Calc. Seq. Length (0) differ	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
162	Entered (18) and Calc. Seq. Length (0) differ	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
182	Entered (1845) and Calc. Seq. Length (0) differ	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
521	Entered (1848) and Calc. Seq. Length (0) differ	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

SEQUENCE MISSING ITEM REPORT PATENT APPLICATION US/08/113,561

DATE: 09/07/93 TIME: 10:42:21

INPUT SET: S1441.raw

APPLICATION NUMBER FILING DATE PRIOR APPLICATION DATA

SEQUENCE CORRECTION REPORT PATENT APPLICATION US/08/113,561

DATE: 09/07/93 TIME: 10:42:21

INPUT SET: S1441.raw

Line

Original Text

Corrected Text

5

(i) APPLICANTS: Adams, Thomas R. et al.

(i) APPLICANT: Adams, Thomas R. et al.